

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2005, 18:49:35 ; Search time 2981 Seconds

(without alignments)
2212.543 Million cell updates/sec

Title: US-10-804-491-25

Sequence: 1 MCKGLAALHSHCLERAKKX.....MCKDSLPRVRSFYQELIK 181

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_p2n.model -DEV=xlp
-Q=cgnt2_1/USPTO.spool_p/US10804491/runat.07012005.093054.7744/app.query.fasta_1.327
-DB=EST -QFMT=fastap -SUFFIX=est -MIMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdt -LIST=45
-DOCALIGN=200 -THR SCORE=dot -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NORM=2ct -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10804491_@CGN_1_1_5180_@runat.07012005.093054.7744 -NCPU=6 -ICPU=3
-NO MAP -LANG=QUEURY -NEG SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_ges1.*
9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	931	100.0	583	CA773163	CA773163 im60e01.y
2	931	100.0	584	CK818116	CK818116 ic19d08.x
3	931	100.0	585	CA948732	CA948732 iq27a04.y
4	931	100.0	614	CA951023	CA951023 it93h02.y
5	931	100.0	631	BM503802	BM503802 ig96a05.y
6	931	100.0	632	BO776798	BO776798 i133d02.y
7	931	100.0	633	CA841290	CA841290 ip32c06.y
8	931	100.0	641	BT1713756	BT1713756 ie03f03.y
9	931	100.0	645	CA394466	CA394466 cs51h05.y

10	931	100.0	645	CA397513	CA397513 cs92a10.y
11	931	100.0	651	CB053503	CB053503 NISC.g114
12	931	100.0	653	BU785180	BU785180 in42509.y
13	931	100.0	661	BE890175	BE890175 601513155
14	931	100.0	695	CN268954	CN268954 170006000
15	931	100.0	696	AU139601	AU139601 1003415.H
16	931	100.0	708	CA407266	CA407266 1003415.H
17	931	100.0	708	CD242148	CD242148 AGENCOURT
18	931	100.0	714	CB962876	CB962876 AGENCOURT
19	931	100.0	718	CA391795	CA391795 cs19a01.y
20	931	100.0	722	CB962581	CB962581 AGENCOURT
21	931	100.0	733	BU539966	BU539966 AGENCOURT
22	931	100.0	734	CD299504	CD299504 AGENCOURT
23	931	100.0	734	CD357245	CD357245 AGENCOURT
24	931	100.0	737	BT770010	BT770010 603053514
25	931	100.0	737	CD000470	CD000470 AGENCOURT
26	931	100.0	738	CD299098	CD299098 AGENCOURT
27	931	100.0	740	CD110719	CD110719 AGENCOURT
28	931	100.0	742	CN268951	CN268951 170005321
29	931	100.0	744	CD511422	CD511422 AGENCOURT
30	931	100.0	746	CB963796	CB963796 AGENCOURT
31	931	100.0	746	CD250671	CD250671 AGENCOURT
32	931	100.0	748	BT082334	BT082334 602671755
33	931	100.0	748	CD299067	CD299067 AGENCOURT
34	931	100.0	749	AU138261	AU138261 170005321
35	931	100.0	751	CB962349	CB962349 AGENCOURT
36	931	100.0	752	CD511304	CD511304 AGENCOURT
37	931	100.0	753	CB963300	CB963300 AGENCOURT
38	931	100.0	756	CB963443	CB963443 AGENCOURT
39	931	100.0	757	CD241903	CD241903 AGENCOURT
40	931	100.0	758	CD356513	CD356513 AGENCOURT
41	931	100.0	759	CB962257	CB962257 AGENCOURT
42	931	100.0	762	CD356626	CD356626 AGENCOURT
43	931	100.0	763	CB963030	CB963030 AGENCOURT
44	931	100.0	765	CN268950	CN268950 170004245
45	931	100.0	766	CB962986	CB962986 AGENCOURT

ALIGNMENTS

RESULT 1
CA773163
LOCUS
DEFINITION
CA773163 583 bp mRNA linear EST 03-DEC-2002
im60e01.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6039624 5'
similar to SW:RG55_HUMAN O15539 REGULATOR OF G-PROTEIN SIGNALING 5'
; mRNA sequence.

ACCESSION
CA773163
VERSION
CA773163.1 GI:26010458
KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scares, M., Brestelli, D., Gradwohl, G., Clifton, S.,
Hillier, L., Maira, M., Pape, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@bioh.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2005, 20:02:25 ; Search time 446 Seconds

(without alignments)
2331.852 Million cell updates/sec

Title: US-10-804-491-25

Perfect score: 931
Sequence: 1 MCKGALPHSCLEPAKELK.....MEKSLPRVSEFYQELIK 181

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL-frame_plus_p2n.model -DEV-x1p
-O=/cgn2_1/USPTO_epool_p/US10804491/runat_07012005_093056_7844/app_query.fasta_1.327
-DB=Published Applications NA -OPMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10804491@CGN 1.1 723 @runat_07012005_093056_7844
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US12_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US13_PUBCOMB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US14_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US15_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/2/pubpna/US25_PUBCOMB.seq.*
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21: /cgn2_6/ptodata/2/pubpna/US27_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	931	100.0	744	9 US-09-206-639-2	Sequence 2, Appl1
2	931	100.0	1691	17 US-10-804-491-24	Sequence 24, Appl1
3	931	100.0	1923	15 US-10-411-224-55	Sequence 55, Appl1
4	931	100.0	1923	16 US-10-047-021-55	Sequence 55, Appl1
5	931	100.0	2076	16 US-10-240-425-345	Sequence 345, Appl1
6	931	100.0	2190	16 US-10-641-643-795	Sequence 795, Appl1
7	918	98.6	5809	15 US-10-133-013-103	Sequence 103, Appl1
8	838	90.0	5443	15 US-10-398-953-2	Sequence 2, Appl1
9	838	90.0	817	15 US-10-398-953-6	Sequence 6, Appl1
10	661	71.0	663	16 US-10-357-820-47	Sequence 47, Appl1
11	637	68.4	459	10 US-09-918-995-17301	Sequence 17301, A
12	584	62.7	411	10 US-09-918-995-17322	Sequence 17322, A
13	499	53.6	800	16 US-10-305-720-1091	Sequence 1091, Ap
14	499	53.6	1531	14 US-10-198-846-9863	Sequence 9863, Ap
15	499	53.6	1869	14 US-10-175-523-144	Sequence 144, App
16	499	53.6	2752	14 US-10-198-846-13843	Sequence 13843, A
17	499	53.6	2934	10 US-09-939-209A-1	Sequence 1, Appl1
18	499	53.6	3165	13 US-10-044-090-113	Sequence 113, App
19	499	53.6	3167	10 US-09-918-624B-6	Sequence 6, Appl1
20	463.5	49.8	2383	14 US-10-171-311-201	Sequence 201, App
21	463.5	49.8	2383	16 US-10-159-563-311	Sequence 311, App
22	462.5	49.7	746	9 US-09-873-438-3	Sequence 3, Appl1
23	462.5	49.7	875	15 US-10-755-889-7	Sequence 7, Appl1
24	462.5	49.7	2434	15 US-10-240-965-112	Sequence 112, App
25	462.5	49.7	2883	18 US-10-723-860-666	Sequence 666, App
26	461	49.5	939	16 US-10-302-172-353	Sequence 353, App
27	459	49.3	540	15 US-10-875-555-1	Sequence 1, Appl1
28	447	48.0	2272	9 US-09-873-438-1	Sequence 1, Appl1
29	445.5	47.9	1697	15 US-10-094-749-11	Sequence 11, Appl1
30	444.5	47.7	3594	13 US-10-087-192-1727	Sequence 1727, Ap
31	443	47.6	1283	16 US-10-814-353-19578	Sequence 19578, A
32	440.5	47.3	2623	16 US-10-108-260A-1527	Sequence 1527, Ap
33	440.5	47.3	2638	9 US-09-954-456-1955	Sequence 1955, Ap
34	440.5	47.3	2638	16 US-10-873-367C-1040	Sequence 1040, Ap
35	440.5	47.3	2638	16 US-10-428-487-113	Sequence 13, Appl1
36	440.5	47.3	2638	16 US-10-305-720-1090	Sequence 1090, Ap
37	440.5	47.3	2638	16 US-10-240-425-1426	Sequence 1426, Ap
38	440.5	47.3	4270	16 US-10-723-860-5665	Sequence 5665, Ap
39	427.5	45.9	1164	9 US-09-894-749-3	Sequence 3, Appl1
40	423	45.4	2874	16 US-10-114-270-151	Sequence 151, App
41	421.5	45.3	848	9 US-09-867-550-847	Sequence 847, App
42	421.5	45.3	1629	16 US-10-191-803-244	Sequence 244, App
43	421.5	45.3	1629	16 US-10-152-312A-1995	Sequence 1995, Ap
44	421.5	45.3	1840	16 US-10-258-371B-18	Sequence 18, Appl1
45	421.5	45.3	1884	17 US-10-115-635-133	Sequence 133, App

ALIGNMENTS

RESULT 1
US-09-206-639-2
Sequence 2, Application US/09206639
Patent No. US20020034777A1

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2005, 19:08:15 ; Search time 87 Seconds

(without alignment)
1478,768 Million cell updates/sec

Title: US-10-804-491-25

Perfect score: 931
Sequence: 1 MCKGLALPHSCLERAKKIK.....MEKDSLPRVSEFYQELIK 181

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlp
-O=/cgn2_1/USPTO.spool.p/US10804491/rn1at 07012005 093055 7757/app.query.fasta_1.327
-DB=Issued Patents NA -QFMT=fastp -SUFFIX=rn1 -MINMATCH=0.1 -IOBCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGQUERY -NEG.SCORES=0 -WAIT -DISPATCH=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6C.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	931	100.0	744	2	US-08-748-483-2
2	931	100.0	1691	4	US-09-709-103-24
3	931	100.0	1691	4	US-09-439-410A-24
4	931	100.0	2190	4	US-09-023-655-795
5	918	98.6	3208	4	US-09-566-921-111
6	499	53.6	800	4	US-09-016-434-1091
7	463.5	49.8	2383	1	US-08-274-318-1
8	463.5	49.8	2383	2	US-08-754-108-1
9	462.5	49.7	606	2	US-08-463-081B-27
10	462.5	49.7	606	2	US-08-461-379A-27
11	462.5	49.7	606	2	US-08-462-390B-27
12	462.5	49.7	606	3	US-08-463-074B-27

13	462.5	49.7	606	3	US-08-465-585C-27	Sequence 27, Appl
14	462.5	49.7 <td>606</td> <td>3<th>US-08-652-446-27</th><th>Sequence 27, Appl</th></td>	606	3 <th>US-08-652-446-27</th> <th>Sequence 27, Appl</th>	US-08-652-446-27	Sequence 27, Appl
15	462.5	49.7 <td>746</td> <td>3<th>US-08-870-815-3</th><th>Sequence 3, Appl</th></td>	746	3 <th>US-08-870-815-3</th> <th>Sequence 3, Appl</th>	US-08-870-815-3	Sequence 3, Appl
16	462.5	49.7 <td>746</td> <td>3<th>US-08-949-004-3</th><th>Sequence 3, Appl</th></td>	746	3 <th>US-08-949-004-3</th> <th>Sequence 3, Appl</th>	US-08-949-004-3	Sequence 3, Appl
17	462.5	49.7 <td>2406</td> <td>2<th>US-08-463-081B-1</th><th>Sequence 1, Appl</th></td>	2406	2 <th>US-08-463-081B-1</th> <th>Sequence 1, Appl</th>	US-08-463-081B-1	Sequence 1, Appl
18	462.5	49.7 <td>2406</td> <td>2<th>US-08-461-379A-1</th><th>Sequence 1, Appl</th></td>	2406	2 <th>US-08-461-379A-1</th> <th>Sequence 1, Appl</th>	US-08-461-379A-1	Sequence 1, Appl
19	462.5	49.7 <td>2406</td> <td>2<th>US-08-462-350B-1</th><th>Sequence 1, Appl</th></td>	2406	2 <th>US-08-462-350B-1</th> <th>Sequence 1, Appl</th>	US-08-462-350B-1	Sequence 1, Appl
20	462.5	49.7 <td>2406</td> <td>3<th>US-08-463-074B-1</th><th>Sequence 1, Appl</th></td>	2406	3 <th>US-08-463-074B-1</th> <th>Sequence 1, Appl</th>	US-08-463-074B-1	Sequence 1, Appl
21	462.5	49.7 <td>2406</td> <td>3<th>US-08-465-585C-1</th><th>Sequence 1, Appl</th></td>	2406	3 <th>US-08-465-585C-1</th> <th>Sequence 1, Appl</th>	US-08-465-585C-1	Sequence 1, Appl
22	462.5	49.7 <td>2406</td> <td>3<th>US-08-652-446-1</th><th>Sequence 1, Appl</th></td>	2406	3 <th>US-08-652-446-1</th> <th>Sequence 1, Appl</th>	US-08-652-446-1	Sequence 1, Appl
23	461	49.5 <td>939</td> <td>4<th>US-09-799-451-353</th><th>Sequence 353, App</th></td>	939	4 <th>US-09-799-451-353</th> <th>Sequence 353, App</th>	US-09-799-451-353	Sequence 353, App
24	447	48.0 <td>2272</td> <td>2<th>US-08-728-228-1</th><th>Sequence 1, Appl</th></td>	2272	2 <th>US-08-728-228-1</th> <th>Sequence 1, Appl</th>	US-08-728-228-1	Sequence 1, Appl
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26	447	48.0 <td>2272</td> <td>3<th>US-08-949-004-1</th><th>Sequence 1, Appl</th></td>	2272	3 <th>US-08-949-004-1</th> <th>Sequence 1, Appl</th>	US-08-949-004-1	Sequence 1, Appl
27	440.5	47.3 <td>2638</td> <td>4<th>US-09-016-434-1090</th><th>Sequence 1090, Ap</th></td>	2638	4 <th>US-09-016-434-1090</th> <th>Sequence 1090, Ap</th>	US-09-016-434-1090	Sequence 1090, Ap
28	427.5	45.9 <td>1164</td> <td>4<th>US-09-244-314-3</th><th>Sequence 3, Appl</th></td>	1164	4 <th>US-09-244-314-3</th> <th>Sequence 3, Appl</th>	US-09-244-314-3	Sequence 3, Appl
29	427.5	45.9 <td>1164</td> <td>4<th>US-09-498-959-3</th><th>Sequence 3, Appl</th></td>	1164	4 <th>US-09-498-959-3</th> <th>Sequence 3, Appl</th>	US-09-498-959-3	Sequence 3, Appl
30	421.5	45.3 <td>2217</td> <td>3<th>US-09-244-314-1</th><th>Sequence 1, Appl</th></td>	2217	3 <th>US-09-244-314-1</th> <th>Sequence 1, Appl</th>	US-09-244-314-1	Sequence 1, Appl
31	421.5	45.3 <td>2217</td> <td>4<th>US-09-498-959-1</th><th>Sequence 1, Appl</th></td>	2217	4 <th>US-09-498-959-1</th> <th>Sequence 1, Appl</th>	US-09-498-959-1	Sequence 1, Appl
32	415.5	44.6 <td>1345</td> <td>4<th>US-09-016-434-1278</th><th>Sequence 1278, Ap</th></td>	1345	4 <th>US-09-016-434-1278</th> <th>Sequence 1278, Ap</th>	US-09-016-434-1278	Sequence 1278, Ap
33	415.5	44.6 <td>1345</td> <td>4<th>US-09-023-655-1243</th><th>Sequence 1243, Ap</th></td>	1345	4 <th>US-09-023-655-1243</th> <th>Sequence 1243, Ap</th>	US-09-023-655-1243	Sequence 1243, Ap
34	351.5	37.8 <td>1398</td> <td>4<th>US-09-016-434-1290</th><th>Sequence 1290, Ap</th></td>	1398	4 <th>US-09-016-434-1290</th> <th>Sequence 1290, Ap</th>	US-09-016-434-1290	Sequence 1290, Ap
35	351.5	37.8 <td>1398</td> <td>4<th>US-09-702-705-322</th><th>Sequence 322, App</th></td>	1398	4 <th>US-09-702-705-322</th> <th>Sequence 322, App</th>	US-09-702-705-322	Sequence 322, App
36	351.5	37.8 <td>1398</td> <td>4<th>US-09-736-457-322</th><th>Sequence 322, App</th></td>	1398	4 <th>US-09-736-457-322</th> <th>Sequence 322, App</th>	US-09-736-457-322	Sequence 322, App
37	351.5	37.8 <td>1398</td> <td>4<th>US-09-614-148-322</th><th>Sequence 322, App</th></td>	1398	4 <th>US-09-614-148-322</th> <th>Sequence 322, App</th>	US-09-614-148-322	Sequence 322, App
38	351.5	37.8 <td>1398</td> <td>4<th>US-09-671-335-322</th><th>Sequence 322, App</th></td>	1398	4 <th>US-09-671-335-322</th> <th>Sequence 322, App</th>	US-09-671-335-322	Sequence 322, App
39	351.5	37.8 <td>1398</td> <td>4<th>US-09-589-184-322</th><th>Sequence 322, App</th></td>	1398	4 <th>US-09-589-184-322</th> <th>Sequence 322, App</th>	US-09-589-184-322	Sequence 322, App
40	351.5	37.8 <td>1398</td> <td>4<th>US-09-658-824-322</th><th>Sequence 322, App</th></td>	1398	4 <th>US-09-658-824-322</th> <th>Sequence 322, App</th>	US-09-658-824-322	Sequence 322, App
41	318	34.2 <td>981</td> <td>2<th>US-08-829-110-2</th><th>Sequence 2, Appl</th></td>	981	2 <th>US-08-829-110-2</th> <th>Sequence 2, Appl</th>	US-08-829-110-2	Sequence 2, Appl
42	318	34.2 <td>981</td> <td>4<th>US-09-016-434-240</th><th>Sequence 240, App</th></td>	981	4 <th>US-09-016-434-240</th> <th>Sequence 240, App</th>	US-09-016-434-240	Sequence 240, App
43	309	33.2 <td>201</td> <td>2<th>US-08-588-258B-20</th><th>Sequence 20, Appl</th></td>	201	2 <th>US-08-588-258B-20</th> <th>Sequence 20, Appl</th>	US-08-588-258B-20	Sequence 20, Appl
44	309	33.2 <td>201</td> <td>3<th>US-08-460-505-20</th><th>Sequence 20, Appl</th></td>	201	3 <th>US-08-460-505-20</th> <th>Sequence 20, Appl</th>	US-08-460-505-20	Sequence 20, Appl
45	309	33.2 <td>201</td> <td>5<th>PCT-US96-08295-20</th><th>Sequence 20, Appl</th></td>	201	5 <th>PCT-US96-08295-20</th> <th>Sequence 20, Appl</th>	PCT-US96-08295-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-748-483-2
Sequence 2, Application US/08748483
Patent No. 5955314
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,483
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0157 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2005, 18:40:14 ; Search time 2732 Seconds
(without alignments)
3133.029 Million cell updates/sec

Title: US-10-804-491-25

Perfect score: 931
Sequence: 1 MCKGLAALPHSCLERAKKXK.....MEKSLPRFVSEPEYQELIK 181

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=xlp
-O=/cgn2_1/USPTO_spool_p/US10804491/runat_07012005_093054_7731/app_query.fasta_1.327
-DB=genemb1 -OEMT=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biocsum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10804491_@CGN_1_1.5600@runat_07012005_093054_7731 -NCPU=6 -ICPU=3
-NO MAP -LARGESUBSTR -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmb1.*
1: gb_da.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_pi.*
8: gb_pi.*
9: gb_pi.*
10: gb_pi.*
11: gb_pi.*
12: gb_pi.*
13: gb_pi.*
14: gb_pi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	931	100.0	546	AF493929 Homo sapi
2	931	100.0	744	AR075100 Sequence
3	931	100.0	744	BD091623 Human reg
4	931	100.0	1285	AF030108 Homo sapi

5	931	100.0	1691	AF159570	AF159570 Homo sapi
6	931	100.0	1710	BC030059	BC030059 Homo sapi
7	931	100.0	1923	BD074349	BD074349 50 human
8	931	100.0	2075	CO714475	CO714475 Sequence
9	931	100.0	2076	AB008109	AB008109 Homo sapi
10	931	100.0	2190	AR380250	AR380250 Homo sapi
11	931	100.0	2601	BV180396	BV180396 sqm10933
12	931	100.0	5683	HSMB05729	BX537427 Homo sapi
13	918	98.6	3208	AR454638	AR454638 Sequence
14	915	98.3	955	BD021618	BD021618 Sequence
15	915	98.3	955	BD101556	BD101556 Novel gen
16	855	91.8	2078	SCC549925	AJ549925 Sus scrofa
17	843	90.5	1812	BC037683	BC037683 Mus muscu
18	838	90.0	543	BD183821	BD183821 New dieea
19	838	90.0	546	AF241259	AF241259 Rattus no
20	838	90.0	546	AF241259	AF241259 Rattus no
21	838	90.0	817	BD183825	BD183825 New dieea
22	838	90.0	817	BD183825	BD183825 New dieea
23	833	89.5	2397	MM067188	U67188 Mus musculu
24	788	84.6	1219	BX931079	BX931079 Gallus ga
25	767	82.4	4487	BC077275	BC077275 Xenopus 1
26	680.5	73.1	2765	BC054594	BC054594 Dario rer
27	510	54.8	2112	BX950639	BX950639 Gallus ga
28	499	53.6	618	AF493928	AF493928 Homo sapi
29	499	53.6	618	BT007025	BT007025 Homo sapi
30	499	53.6	618	BT007756	BT007756 Synthetic
31	499	53.6	800	AR270528	AR270528 Sequence
32	499	53.6	800	HSU27768	U27768 Human RGP4
33	499	53.6	840	CO714476	CO714476 Sequence
34	499	53.6	1238	CO434203	CO434203 Sequence
35	499	53.6	1869	BC000737	BC000737 Homo sapi
36	499	53.6	2753	BC051869	BC051869 Homo sapi
37	499	53.6	2934	AX451335	AX451335 Sequence
38	497	53.4	1489	RNU27767	U27767 Rattus norv
39	497	53.4	2919	AF117211	AF117211 Rattus nor
40	496.5	53.3	2214	AY297457	AY297457 Gallus ga
41	494	53.1	2114	BC055293	BC055293 Mus muscu
42	494	53.1	2781	BC003882	BC003882 Mus muscu
43	491	52.7	630	AB004315	AB004315 Mus muscu
44	473.5	50.9	1651	BC064234	BC064234 Xenopus t
45	468.5	50.3	606	MMU0427	U70427 Mus musculu

ALIGNMENTS

RESULT 1	AF493929	546 bp	mRNA	linear	PRI 14-APR-2002
LOCUS	AF493929				
DEFINITION	Homo sapiens regulator of G protein signalling 5 (RGSS5) mRNA,				
ACCESSION	AF493929				
VERSION	AF493929.1	GI:20147750			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Publ.H.L. Iii, Ikeda.S.R. and Aronstam.R.S.				
TITLE	Regulator of G protein signalling 5 (RGSS5), human				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 546)				
TITLE	Publ.H.L. Iii, Ikeda.S.R. and Aronstam.R.S.				
JOURNAL	Direct Submission				
FEATURES	Submitted (21-MAR-2002) CDNA Resource Center, Guthrie Research Institute, One Guthrie Square, Sayre, PA 18840, USA				
SOURCE	Location/Qualifiers				
	1..546				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:550112"				
	1..546				

gene

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2005, 18:39:04 ; Search time 421 Seconds
(without alignments)
2256.877 Million cell updates/sec

Title: US-10-804-491-25

Sequence: 1 MCKGAALPHSCLERAERIK.....MERKSLPRFVSEFYOLIK 181

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=firex+ p2n.model -DEV=xlp
-Q/cgml 1/USPTO.spool.p/US10804491/rnat.07012005.093053.7724/app.query.fasta.1.327
-DB=N.Geneseq.23Sep04 -QFMT=fastap -SUFFIX=mg -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10804491 @CGN 1.1 708 @rnat.07012005.093053.7724 -MCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq.23Sep04:*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn20018:*
5: geneseqn20018s:*
6: geneseqn20028s:*
7: geneseqn20038s:*
8: geneseqn20038s:*
9: geneseqn20038s:*
10: geneseqn20038s:*
11: geneseqn20038s:*
12: geneseqn20048s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	931	100.0	745	2	AAV38084 Human reg
2	931	100.0	1691	3	AAZ36910 CDNA enco
3	931	100.0	1923	6	AAx51745 DNA enco
4	931	100.0	1923	6	ABO92597 Human sec
5	931	100.0	2075	10	ABX74396 Human CDN
6	931	100.0	2076	11	ADP65641 Human mRN

7	931	100.0	2076	11	ADP65077 Human reg
8	931	100.0	2190	11	AD131469 Human CDN
9	918	98.6	3208	12	AD161743 Human CDN
10	918	98.6	5809	10	AD102562 Human CDN
11	915	98.3	955	4	AA197781 Human neu
12	838	90.0	543	6	AB199975 Rat disea
13	838	90.0	817	6	AB199975 Rat disea
14	661	71.0	663	10	ADP44700 Human NOV
15	645	69.3	663	12	AD050885 Human NOV
16	637	68.4	459	9	ACH26489 Human adu
17	584	62.7	411	9	ACH29910 Human tes
18	499	53.6	753	11	ADN95589 Human BEC
19	499	53.6	800	10	ACA56493 Human sig
20	499	53.6	800	12	AD156289 Human pol
21	499	53.6	1238	4	AA126766 Human bre
22	499	53.6	2769	12	ADP21408 Gene RGS4
23	499	53.6	2934	6	ABK47336 CDNA enco
24	499	53.6	3165	8	ABX63113 Human CDN
25	499	53.6	3167	10	AD126660 Human CDN
26	496	53.3	558	10	ADB57446 Toxicity
27	463.5	49.8	2383	8	AA114148 p53 reppo
28	463.5	49.8	2383	8	ACP12929 Human cer
29	463.5	49.8	2383	10	ADK61425 Ovarian c
30	463.5	49.8	2383	11	ADN95175 Human BEC
31	463.5	49.8	2383	12	ADOL19709 Human PRO
32	463.5	49.8	2383	12	ADOL19707 Human PRO
33	462.5	49.7	606	3	AAA39678 Cytochrome
34	462.5	49.7	746	2	AAV34780 Human RAT
35	462.5	49.7	2132	12	ADP21402 Gene RGS1
36	462.5	49.7	2406	2	AA143376 Human cyt
37	462.5	49.7	2406	3	AA39660 Human CR1
38	462.5	49.7	2434	6	AA594857 Human DNA
39	462.5	49.7	2883	12	ADQ23786 Human sof
40	461	49.5	939	6	AB11471 Human pol
41	461	49.5	939	12	ADMA4389 Novel hum
42	459	48.3	540	6	AB92505 Human reg
43	456	48.0	597	5	AA57442 Human RGS
44	455	48.9	2272	2	AAV34779 Mouse RAT
45	445.5	47.9	1697	10	ADA52443 Human cod

ALIGNMENTS

RESULT 1	AAV38084	AAV38084 strand; CDNA; 745 BP.
ID	AAV38084	
AC	AAV38084	
XX		
DT	14-SEP-1998	(first entry)
DE		Human regulator of G-protein signalling encoding CDNA.
XX		
KM		Human; regulator; G-protein signalling; HRGS; cancer; inflammation;
KW		hypertension; cardiovascular shock; arrhythmias; asthma; ss.
OS		Homo sapiens.
XX		
FT	Key	Location/Qualifiers
FT	CDS	70..615
FT		/*tag= a
FT		/product= "regulator of G-protein signalling"
PD	MO9820128-A1.	
XX		
PF	14-MAY-1998.	
XX		
PR	06-NOV-1997;	97WO-US018476.
XX		
PR	08-NOV-1996;	96US-00748483.
XX		
PA	(INCY-)	INCYTE PHARM INC.
XX		

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OM protein - protein search, using sw model

Run on: January 12, 2005, 16:32:21 ; Search time 74.0455 Seconds
(without alignments)
1406.471 Million cell updates/sec

Title: US-10-804-491-25
Perfect score: 931
Sequence: 1 MCKGLALPHSCLEPRAKEIK.....MEKSLPRFVSEFYQELIK 181

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02 :
1: uniprot_sprot :
2: uniprot_trembl :*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	931	100.0	181	1	RGSS_HUMAN
2	931	100.0	181	1	CAD97669
3	855	91.8	181	2	Q86422
4	843	90.5	181	1	RGSS_MOUSE
5	843	90.5	181	2	BAC31773
6	843	90.5	181	2	BAC35555
7	838	90.0	181	1	RGSS_RAT
8	767	82.4	181	2	Q6D667
9	680.5	73.1	182	2	Q7D2D3
10	499	53.6	205	1	RGSS_HUMAN
11	499	53.6	205	2	AAP35671
12	497	53.4	205	1	RGSS_RAT
13	496.5	53.3	205	2	Q7S2C6
14	494	53.1	205	2	AAP35293
15	494	53.1	205	2	BAC27009
16	494	53.1	205	2	BAC30249
17	491	52.7	205	1	RGSS_MOUSE
18	473.5	50.9	205	2	Q6P3T0
19	472.5	50.9	205	2	AAP35234
20	462.5	49.7	202	1	RGSS_HUMAN
21	462.5	49.7	202	1	AAP35284
22	461.5	49.6	202	1	RGSS_BOVIN
23	459	49.3	180	1	RGSS_HUMAN
24	459	49.3	180	2	AAP35677
25	456.5	49.0	204	2	Q919D9
26	456	49.0	180	1	RGSS_RAT
27	456	49.0	198	1	AAP35284
28	455	48.9	201	1	RGSS_MOUSE
29	455	48.9	201	2	Q7D2D3
30	455	48.9	201	2	BAC37678
31	453	48.7	174	2	Q6D667

32	452	48.5	180	2	OBX1
33	452	48.5	180	2	AAP35056
34	451	48.4	199	1	RGSS_RAT
35	449	48.2	196	2	Q95K68
36	445.5	47.9	192	2	Q6WV93
37	445.5	47.9	184	2	Q6WV93
38	443.5	47.6	174	2	Q6WV02
39	443.5	47.6	319	2	Q6WV02
40	440.5	47.3	519	1	RGSS_HUMAN
41	440.5	47.3	917	2	Q6WV02
42	440.5	47.3	917	2	Q6WV02
43	440.5	47.3	917	2	Q6WV02
44	440.5	47.3	1093	2	Q6WV02
45	440.5	47.3	1198	2	Q6WV02

ALIGNMENTS

RESULT 1

ID RGSS_HUMAN STANDARD: PRT: 181 AA.

AC O15539;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Regulator of G-protein signaling 5 (RGSS).
GN Name=RGSS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chatterjee T.K., Fisher R.A.,
RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuroblastoma;
RX MEDLINE=98419174; PubMed=9747037;
RA Seki N., Sugano S., Suzuki Y.-I., Nakagawara A., Ohira M.,
RT Muramatsu M., Saito T., Hori T.,
RT "Isolation, tissue expression, and chromosomal assignment of human
RGSS, a novel G-protein signaling regulator gene.";
RL J. Hum. Genet. 43:202-205(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=99403338; PubMed=10471929;
RA Cierniewski M.J., Takesono A., Ma C., Lizano J.S., Xie X.,
RT Fuernkrantz H., Lanier S.M., Duzic E.,
RT "Genetic screens in yeast to identify mammalian nonreceptor modulators
of G-protein signaling.";
RL Nat. Biotechnol. 17:878-883(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Pull H.L., Ili, Ikeda S.R., Aronson R.S.,
RT "cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org)."
RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stedman M., Soares M.B., Bonaldon M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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OM protein - protein search, using sw model

Run on: January 12, 2005, 16:38:13 ; Search time 18.0216 Seconds
(without alignments)
966.351 Million cell updates/sec

Title: US-10-804-491-25

Perfect score: 931
Sequence: 1 MCKGLAALPHSCLERAKEIK.....MEKDSLPRFVSEFYQELIK 181

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	758	81.4	181	2 JC7228	G-protein signalin
2	499	53.6	205	2 S78221	G-protein signalin
3	440.5	47.3	519	2 S78089	G-protein signalin
4	415.5	44.6	211	2 IS3020	G-0/G-1 switch reg
5	349.5	37.5	196	2 S43436	B cell activation
6	297	31.9	244	2 T13580	hypothetical prote
7	294	31.6	251	2 S43576	COSB5.7 protein (c
8	294	31.6	254	2 G88571	protein COSB5.7 [i
9	287	30.8	181	2 T21035	hypothetical prote
10	282	30.3	533	2 T31002	hypothetical prote
11	281	30.2	169	2 T21034	hypothetical prote
12	255.5	27.4	173	2 S71812	RGS10 protein - hu
13	232.5	25.0	544	2 JC5503	G-protein signalin
14	222	23.8	558	2 T21468	hypothetical prote
15	214	23.0	234	2 T26672	hypothetical prote
16	213	22.9	473	2 T19337	hypothetical prote
17	197.5	21.2	1387	2 JC5502	G-protein signalin
18	196.5	21.1	832	2 T08422	negative regulator
19	165	17.7	270	2 T22213	hypothetical prote
20	162.5	17.5	274	2 T22214	hypothetical prote
21	159	17.1	838	2 T08423	Axin homolog Axil
22	150	16.1	719	2 S60771	developmental regu
23	149	16.0	303	2 T29513	hypothetical prote
24	141.5	15.2	235	2 F89472	protein ZC53.7 [im
25	134.5	14.4	284	2 T15700	hypothetical prote
26	127.5	13.7	309	2 S61665	probable membrane
27	114	12.2	229	2 A89473	protein F52D2.2 [i
28	105	11.3	1260	2 T20487	hypothetical prote
29	101.5	10.9	657	2 H86344	T2111.1 protein -

30	101	10.8	1620	2 S61535	nucleotide-binding
31	98.5	10.6	492	2 A61382	phosphorylation re
32	98	10.5	913	2 T31497	hypothetical prote
33	96.5	10.4	1085	2 C96797	unknown protein [i
34	96	10.3	688	1 JC1469	beta-adrenergic-re
35	94	10.1	507	2 C82901	conserved hypothet
36	93	10.0	157	2 G64540	hypothetical prote
37	93	10.0	400	2 E70318	hypothetical prote
38	93	10.0	465	2 D81312	hypothetical prote
39	93	10.0	688	1 A39336	beta-adrenergic-re
40	92.5	9.9	367	2 E81060	conserved hypothet
41	92.5	9.9	395	2 E81805	hypothetical prote
42	92.5	9.9	1046	2 A86790	ATP-dependent dABN
43	91.5	9.8	688	1 T73628	beta-adrenergic-re
44	90	9.7	728	2 A81385	probable ATP /GTP
45	89.5	9.6	2774	2 A43359	microtubule-associ

ALIGNMENTS

RESULT 1

UC7228 G-protein signaling regulator 5 homolog - clawed frog

C/Species: Xenopus sp. (Clawed frog)

C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000

C/Accession: JC7228; PC7066

R/Saitoh, O.; Odagiri, M.; Masuno, I.; Nomoto, S.; Kinoshita, N.

Biochem. Biophys. Res. Commun. 270, 34-39, 2000

A/Title: Molecular cloning and characterization of Xenopus RGS5.

A/Reference number: JC7228

A/Accession: JC7228

A/Molecule type: mRNA

A/Residues: 1-181 <SAI>

A/Accession: PC7066

A/Molecule type: protein

A/Residues: 88-168 <SA2>

A/Experimental source: embryo

C/Comment: This protein has function as a GTPase-activating protein. It interacts with

genesis and cell differentiation.

C/Superfamily: B-cell activation protein BL34

C/Keywords: differentiation; embryo

Query Match	81.4%; Score 758; DB 2; Length 181;
Best Local Similarity	79.0%; Pred. No. 4.4e-52;
Matches 143; Conservative	20; Mismatches 18; Indels 0; Gaps 0;
QY	1 MCKGLAALPHSCLERAKEIKILGILQKPDVGLVFPNKEPKPAKTQTSIDBALQ 60
DB	1 MCKGLAALPHSCLERAKEIKILGILQKPDVGLVFPNKEPKPAKTQTSIDBALQ 60
QY	61 WRDSLDKILNNYGLASFPKSEFSEENLEFWIACEDYKKIKSPAKVAEAKOYIEEF 120
DB	61 WRDSLEKLENSYGLSVFQSLKSEFSEENLEFWIACEDYKKIKSPAKVAEAKOYIEEF 120
QY	121 IQTEAPKEVINIHFTKDTIMKNLVEPSLSPDMAQKRIHALMEKDSLPRFVSEFYQELI 180
DB	121 IQTEAPKEVINIHFTKDTIMKNLVEPSLSPDMAQKRIHALMEKDSLPRFVSEFYQELI 180
QY	181 K 181
DB	181 K 181

RESULT 2

S78221 G-protein signaling regulator RGP4 - human

N/Alternate names: G-protein signaling regulator RGS4

C/Species: Homo sapiens (man)

C/Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C/Accession: S78221; S66509

R/Druy, K.

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OM protein - protein search, using sw model

Run on: January 12, 2005, 18:34:53 ; Search time 436.829 Seconds
(Without alignments)
149.700 Million cell updates/sec

Title: US-10-804-491-25

Sequence: 1 MCKGALALPHSLERAKEIK.....MEXDISPRVSEFYQELIK 181

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	931	100.0	181	15	US-10-258-371B-22
3	931	100.0	181	16	US-10-804-491-25
4	931	100.0	190	14	US-10-411-224-197
5	931	100.0	190	15	US-10-047-021-197
6	838	90.0	181	14	US-10-398-953-1
7	661	71.0	135	15	US-10-357-820-48
8	499	53.6	205	9	US-09-206-639-5
9	499	53.6	205	10	US-09-939-209A-2
10	499	53.6	205	15	US-10-258-371B-21
11	463.5	49.8	202	14	US-10-171-311-202
12	462.5	49.7	202	9	US-09-873-438-4
13	462.5	49.7	202	16	US-10-755-889-8

14	462.5	49.7	204	15	US-10-258-371B-23	Sequence 23, Appl
15	459	49.3	180	14	US-10-275-555-2	Sequence 2, Appl
16	456	49.0	180	15	US-10-258-371B-27	Sequence 27, Appl
17	447	48.0	201	9	US-09-873-438-2	Sequence 2, Appl
18	445.5	47.9	284	14	US-10-094-749-1650	Sequence 1650, Ap
19	444.5	47.7	776	13	US-10-087-192-1728	Sequence 1728, Ap
20	440.5	47.3	519	14	US-10-113-794A-2	Sequence 2, Appl
21	440.5	47.3	519	15	US-10-428-487-14	Sequence 14, Appl
22	440.5	47.3	519	15	US-10-258-371B-28	Sequence 28, Appl
23	440.5	47.3	591	15	US-10-108-260A-3970	Sequence 3970, Ap
24	429.5	46.1	930	14	US-10-113-794A-1	Sequence 1, Appl
25	427.5	45.9	235	9	US-09-894-749-4	Sequence 4, Appl
26	423	45.4	923	15	US-10-114-270-152	Sequence 152, App
27	421.5	45.3	227	9	US-09-867-550-848	Sequence 848, App
28	421.5	45.3	235	9	US-09-894-749-2	Sequence 2, Appl
29	421.5	45.3	235	15	US-10-258-371B-20	Sequence 20, Appl
30	415.5	44.6	211	9	US-09-206-639-4	Sequence 4, Appl
31	415.5	44.6	211	15	US-10-258-371B-24	Sequence 24, Appl
32	415.5	44.6	211	16	US-10-408-765A-493	Sequence 493, App
33	415.5	44.6	220	9	US-09-925-300-1507	Sequence 1507, Ap
34	391	42.0	128	15	US-10-352-843-1	Sequence 1, Appl
35	391	42.0	128	15	US-10-352-843-3	Sequence 3, Appl
36	391	42.0	167	10	US-09-942-055A-1	Sequence 1, Appl
37	351.5	37.8	196	9	US-09-206-639-3	Sequence 339, Appl
38	351.5	37.8	196	9	US-09-736-457-339	Sequence 339, App
39	351.5	37.8	196	9	US-09-902-941-339	Sequence 339, App
40	351.5	37.8	196	9	US-09-849-626-339	Sequence 339, App
41	351.5	37.8	196	10	US-09-476-300-339	Sequence 339, App
42	351.5	37.8	196	14	US-10-017-754-339	Sequence 339, App
43	351.5	37.8	196	14	US-10-113-872-339	Sequence 339, App
44	351.5	37.8	196	14	US-10-247-671-176	Sequence 176, App
45	351.5	37.8	196	14	US-10-283-017-339	Sequence 339, App

ALIGNMENTS

RESULT 1
US-09-206-639-1
Sequence 1, Application US/09206639
Patent No. US20020034777A1
GENERAL INFORMATION:
APPLICANT: Hallman, Jennifer L.
Goli, Surya K.
TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,639
FILING DATE: 07-Dec-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/748,483
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0157 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>

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OM protein - protein search, using sw model

Run on: January 12, 2005, 18:15:29 ; Search time 23.1147 Seconds
(without alignments)
519.304 Million cell updates/sec

Title: US-10-804-491-25

Perfect score: 931

Sequence: 1 MCKGIALPHSCLERAKKIK.....MEKSLPRVRFSEFYQELIK 181

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	607	65.2	120	3	US-08-890-865A-12
5	499	53.6	205	2	US-08-829-110-6
6	499	53.6	205	2	US-08-748-483-5
7	463.5	49.8	202	1	US-08-774-318-2
8	463.5	49.8	202	2	US-08-754-108-2
9	462.5	49.7	202	2	US-08-463-081B-2
10	462.5	49.7	202	2	US-08-463-379A-2
11	462.5	49.7	202	2	US-08-462-390B-2
12	462.5	49.7	202	3	US-08-870-815-4
13	462.5	49.7	202	3	US-08-463-074B-2
14	462.5	49.7	202	3	US-08-465-585C-2
15	462.5	49.7	202	3	US-08-652-446-2
16	462.5	49.7	202	3	US-08-949-004-4
17	462.5	49.7	202	2	US-08-726-228-2
18	447	48.0	201	3	US-08-870-815-2
19	447	48.0	201	3	US-08-949-004-2
20	427.5	45.9	235	3	US-09-244-314-4
21	427.5	45.9	235	3	US-09-498-959-4
22	421.5	45.3	235	4	US-09-244-314-2
23	421.5	45.3	235	4	US-09-498-959-2
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25	384	41.2	120	3	US-08-890-865A-14
26	382	41.0	120	3	US-08-890-865A-11
27	377	40.5	120	3	US-08-890-865A-13

28	374.5	40.2	121	2	US-08-588-258B-32	Sequence 32, Appl
29	374.5	40.2	121	3	US-08-460-505-32	Sequence 32, Appl
30	374.5	40.2	121	5	PCT-US96-08295-32	Sequence 32, Appl
31	351.5	37.8	196	2	US-08-829-110-5	Sequence 3, Appl
32	351.5	37.8	196	2	US-08-748-483-3	Sequence 3, Appl
33	351.5	37.8	196	4	US-09-702-705-339	Sequence 339, App
34	351.5	37.8	196	4	US-09-736-457-339	Sequence 339, App
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36	351.5	37.8	196	4	US-09-671-125-339	Sequence 339, App
37	351.5	37.8	196	4	US-09-588-184-339	Sequence 339, App
38	351.5	37.8	196	4	US-09-658-824-339	Sequence 339, App
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41	325.5	35.0	119	5	PCT-US96-08295-31	Sequence 31, Appl
42	323.5	34.7	119	3	US-08-890-865A-15	Sequence 15, Appl
43	318	34.2	159	2	US-08-829-110-1	Sequence 11, Appl
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ALIGNMENTS

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RESULT 1
US-08-748-483-1
; Sequence 1, Application US/08748483
; Patent No. 5955314
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,483
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0157 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 57362
; US-08-748-483-1
; Query Match 100.0%; Score 931; DB 2; Length 181;
; Best Local Similarity 100.0%; Pred. No. 8.6e-87;
; Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 11:30:02 ; Search time 4859 Seconds

(without alignments)
12681.537 Million cell updates/sec

Title: US-10-804-491-24

Perfect score: 1691
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Scoring table: IDENTITY NUC
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Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	1113.4	65.8	1452	3	CR597576 full-length
5	1079.6	63.8	1147	5	BX425491
6	1079.4	63.8	1101	5	CR609141 full-length
7	1055.2	62.4	1101	5	BX446885
8	1033.6	60.1	1143	5	BX446297
9	1016.8	60.1	1099	1	AL515897
10	1011.4	59.8	1132	5	BX384451
11	1000.4	59.2	1002	5	CR625895
12	990	58.5	1096	5	BX403980
13	985.4	58.3	1000	3	CR617436 full-length
14	973.4	57.6	1092	1	AL517305
15	968	57.2	1177	5	BUS08112
16	958.2	56.7	998	1	AL516736
17	955	56.5	1073	5	BX458066
18	954.8	56.4	1054	5	BX425160
19	954.2	56.4	973	1	AL515896
20	946.4	55.0	1074	5	BX438124
21	945.8	55.0	1125	1	AL514350
22	945	55.9	1129	5	BX403854
23	939	55.5	1065	1	AL517317
24	938.2	55.5	1097	5	BX416594

25	935.2	55.3	1060	1	AL518711
26	932.6	55.2	1101	1	AL518211
27	932.2	55.1	1121	1	AL518726
28	931.4	55.1	1065	5	BX425274
29	928.4	54.9	1066	5	AL515561
30	927	54.8	1061	5	BX425161
31	923	54.6	1182	5	BUS08040
32	921.4	54.5	933	1	AL514762
33	901.6	53.3	1065	1	AL518255
34	896.4	53.0	1068	5	BX457536
35	888.8	52.6	1001	5	BX403989
36	888.6	52.5	990	1	AL514666
37	881.8	52.1	1074	1	AL518459
38	880	52.0	981	5	BQ719360
39	876	51.8	1132	5	BX446626
40	875.2	51.8	1136	1	AL518210
41	875	51.7	894	5	BX404056
42	871.2	51.5	912	1	AL514736
43	868	51.3	881	1	AL514802
44	866.6	51.2	1065	5	BX416045
45	864.8	51.1	1085	5	BX446930

ALIGNMENTS

RESULT 1
LOCUS: CR619141
DEFINITION: full-length cDNA clone CLOBB0112G05 of Neuroblastoma of Homo sapiens (human).
ACCESSION: CR619141
VERSION: CR619141.1 GI:50499948
KEYWORDS: HTC; CNSLT; CDNA.
SOURCE: Homo sapiens (human)
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE: Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE: Full-length cDNA libraries and normalization
JOURNAL: Unpublished
REMARK: Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Paraday Avenue
2 (bases 1 to 1714)
Genoscope.
REFERENCE: Direct Submission
AUTHORS: Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web: www.genoscope.cns.fr
COMMENT: 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBB0112G05"
/tissue="Cloblastoma"
/plasmid="pCMVSPORT_6"

ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1690; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TAAGAAGTTGACTTAAGCGAGAGCTAAGCCACCTGCAAAATGTGCAAGACTTG 60
24 TAAGAAGTTGACTTAAGCGAGAGCTAAGCCACCTGCAAAATGTGCAAGACTTG 83

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 15:05:01 ; Search time 935 Seconds
(without alignments)
10391.762 Million cell updates/sec

Title: US-10-804-491-24

Perfect score: 1691

Sequence: 1 taagaagttgacttaagc.....tgcataaaaaaaaaaaaaa 1691

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications_NA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1689.4	99.9	2076	US-10-240-425-345	Sequence 345, Appl
3	1678.4	99.3	5809	US-10-133-013-103	Sequence 103, Appl
4	1676.4	99.1	1923	US-10-111-224-55	Sequence 55, Appl
5	1676.4	99.1	1923	US-10-047-021-55	Sequence 55, Appl
6	1587.8	93.9	2190	US-10-641-643-795	Sequence 795, Appl
7	856.2	50.6	878	US-09-604-287A-82	Sequence 82, Appl
8	856.2	50.6	878	US-09-834-759-82	Sequence 82, Appl
9	856.2	50.6	878	US-09-339-338-82	Sequence 82, Appl
10	856.2	50.6	878	US-09-551-621-82	Sequence 82, Appl
11	856.2	50.6	878	US-10-007-805-82	Sequence 82, Appl
12	856.2	50.6	878	US-10-076-622-82	Sequence 82, Appl

13	856.2	50.6	878	15	US-10-124-805-82	Sequence 82, Appl
14	856.2	50.6	878	15	US-10-441-893-82	Sequence 82, Appl
15	720	42.6	744	9	US-09-206-639-2	Sequence 2, Appl
16	606.6	35.9	631	9	US-09-736-457-553	Sequence 553, Appl
17	606.6	35.9	631	9	US-09-902-941-553	Sequence 553, Appl
18	606.6	35.9	631	9	US-09-849-626-553	Sequence 553, Appl
19	606.6	35.9	631	10	US-09-476-100-553	Sequence 553, Appl
20	606.6	35.9	631	14	US-10-017-754-553	Sequence 553, Appl
21	606.6	35.9	631	15	US-10-113-872-553	Sequence 553, Appl
22	606.6	35.9	631	15	US-10-283-017-553	Sequence 553, Appl
23	601.4	35.6	607	14	US-10-175-523-35	Sequence 35, Appl
24	572.8	33.9	784	9	US-09-736-457-1658	Sequence 1658, Ap
25	572.8	33.9	784	9	US-09-902-941-1658	Sequence 1658, Ap
26	572.8	33.9	784	9	US-09-849-626-1658	Sequence 1658, Ap
27	572.8	33.9	784	14	US-10-017-754-1658	Sequence 1658, Ap
28	572.8	33.9	784	15	US-10-113-872-1658	Sequence 1658, Ap
29	572.8	33.9	784	15	US-10-283-017-1658	Sequence 1658, Ap
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31	543.4	32.1	576	9	US-09-902-941-657	Sequence 657, App
32	543.4	32.1	576	9	US-09-849-626-657	Sequence 657, App
33	543.4	32.1	576	10	US-09-476-100-657	Sequence 657, App
34	543.4	32.1	576	14	US-10-017-754-657	Sequence 657, App
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37	516.4	30.5	571	11	US-09-969-034-2951	Sequence 2951, Ap
38	491.4	29.1	817	15	US-10-398-953-6	Sequence 6, Appl
39	456	27.0	457	16	US-10-242-535A-42596	Sequence 42596, A
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41	442.8	26.2	543	15	US-10-398-953-2	Sequence 2, Appl
42	426.4	25.2	663	16	US-10-357-820-47	Sequence 47, Appl
43	423.8	25.1	427	10	US-09-918-995-5821	Sequence 5821, Ap
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ALIGNMENTS

RESULT 1
US-10-804-491-24
Sequence 24, Application US/10804491
Publication No. US20040180375A1
GENERAL INFORMATION:
APPLICANT: Cismowski, Mary
APPLICANT: Duzic, Emil
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
FILE REFERENCE: 60388-A-PCT-US
CURRENT FILING DATE: 2004-03-19
PRIORITY FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US/09/709,103
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 1691
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (45)..(587)
OTHER INFORMATION:
US-10-804-491-24

Query Match: 100.0%; Score 1691; DB 17; Length 1691;

Best Local Similarity: 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1691; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CAGCTTCCCTCATGCTGCTGGAAGGCGCAAGAGATTAAATCAAGTTGGCAATTC 120

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OM nucleic - nucleic search, using bw model

Run on: January 12, 2005, 11:46:42 ; Search time 163 Seconds
(without alignments)
7373.890 Million cell updates/sec

Title: US-10-804-491-24

Perfect score: 1691
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
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4	1587.8	93.9	2190	US-09-023-655-795	Sequence 795, App
5	856.2	50.6	878	US-09-232-575-82	Sequence 82, Appl
6	856.2	50.6	878	US-09-389-681-82	Sequence 82, Appl
7	856.2	50.6	878	US-09-620-405B-82	Sequence 82, Appl
8	856.2	50.6	878	US-09-339-338-82	Sequence 82, Appl
9	856.2	50.6	878	US-09-433-826B-82	Sequence 82, Appl
10	856.2	50.6	878	US-09-604-287A-82	Sequence 82, Appl
11	856.2	50.6	878	US-09-285-480-82	Sequence 82, Appl
12	856.2	50.6	878	US-09-834-759-82	Sequence 82, Appl
13	856.2	50.6	878	US-09-590-751A-82	Sequence 82, Appl
14	720	42.6	744	US-08-748-483-2	Sequence 2, Appl
15	606.6	35.9	631	US-09-702-705-553	Sequence 553, App
16	606.6	35.9	631	US-09-736-457-553	Sequence 553, App
17	606.6	35.9	631	US-09-614-124B-553	Sequence 553, App
18	606.6	35.9	631	US-09-671-325-553	Sequence 553, App
19	606.6	35.9	631	US-09-589-184-553	Sequence 553, App
20	606.6	35.9	631	US-09-658-824-553	Sequence 553, App
21	572.8	33.9	784	US-09-702-705-1658	Sequence 1658, Ap
22	572.8	33.9	784	US-09-736-457-1658	Sequence 1658, Ap
23	572.8	33.9	784	US-09-614-124B-1658	Sequence 1658, Ap
24	572.8	33.9	784	US-09-671-325-1658	Sequence 1658, Ap
25	572.8	33.9	784	US-09-589-184-1658	Sequence 1658, Ap
26	543.4	32.1	576	US-09-702-705-657	Sequence 657, App
27	543.4	32.1	576	US-09-736-457-657	Sequence 657, App

28	543.4	32.1	576	US-09-614-124B-657	Sequence 657, App
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31	543.4	32.1	576	US-09-658-824-657	Sequence 657, App
32	379.2	22.4	399	US-09-702-705-491	Sequence 491, App
33	379.2	22.4	399	US-09-736-457-491	Sequence 491, App
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35	379.2	22.4	399	US-09-671-325-491	Sequence 491, App
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37	379.2	22.4	399	US-09-658-824-491	Sequence 491, App
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45	188.6	11.2	746	US-08-870-815-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1	US-09-709-103-24	Sequence 24, Application US/09709103
Patent No. 6733991		
GENERAL INFORMATION:		
APPLICANT: Cismowski, Mary		
APPLICANT: Duzic, Emil		
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor		
FILE REFERENCE: 60388-A-PCT-US		
CURRENT APPLICATION NUMBER: US/09/709,103		
NUMBER OF SEQ ID NOS: 73		
SOFTWARE: PatentIn version 3.1		
SEQ ID NO 24		
LENGTH: 1691		
TYPE: DNA		
ORGANISM: Homo Sapiens		
FEATURE:		
NAME/KEY: CDS		
LOCATION: (45)..(587)		
OTHER INFORMATION:		
US-09-709-103-24		
Query Match	100.0%; Score 1691; DB 4; Length 1691;	
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DB	61	CAGCTTGGCCCACTCATGCTGGAAGGCGCAAGATTAAATCAAGTTGGGAATTC 120
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QY	121	TCTCTCAGAAAGCAAGCTAGTTGGTGCATTTGTCATTCGTCATATGAAAGCCAGAGA 180
DB	121	TCTCTCAGAAAGCAAGCTAGTTGGTGCATTTGTCATTCGTCATATGAAAGCCAGAGA 180
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DB	181	AACCGAGCAAGCCAGAAACCTGCGTGAAGCAAGGCGCTGCAAGTGGGTATTCCTCG 240
QY	181	AACCGAGCAAGCCAGAAACCTGCGTGAAGCAAGGCGCTGCAAGTGGGTATTCCTCG 240
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DB	241	ACAACTCTGAGAACTAGTGAAGCTTCAAAAGTTCTGAAAGTGAAT 300
QY	241	ACAACTCTGAGAACTAGTGAAGCTTCAAAAGTTCTGAAAGTGAAT 300
DB	241	ACAACTCTGAGAACTAGTGAAGCTTCAAAAGTTCTGAAAGTGAAT 300
QY	301	TCAAGTGAAGAACTTGAAGTTGCTGAGAGTTTCAAGAAAGATCAAGTCCC 360
DB	301	TCAAGTGAAGAACTTGAAGTTGCTGAGAGTTTCAAGAAAGATCAAGTCCC 360
QY	301	TCAAGTGAAGAACTTGAAGTTGCTGAGAGTTTCAAGAAAGATCAAGTCCC 360
DB	301	TCAAGTGAAGAACTTGAAGTTGCTGAGAGTTTCAAGAAAGATCAAGTCCC 360

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 03:41:28 ; Search time 788 Seconds
(without alignments)
11264.938 Million cell updates/sec

Title: US-10-804-491-24
Perfect score: 1691
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Scoring table: IDENTITY_NUC
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Searched: 4134886 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772

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Post-processing: Minimum Match 0%
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- 12: geneeqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	1676.4	99.1	1923	2	AAK51745
8	1676.4	99.1	1923	6	ABO92597
9	1587.8	93.9	2180	11	AD131469
10	1633.8	74.7	10427	6	ABK69943
11	856.2	50.6	878	4	AAAF17597
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13	856.2	50.6	878	6	ABK95062
14	856.2	50.6	878	6	ABT08682
15	856.2	50.6	878	6	ABK63626
16	856.2	50.6	878	10	ABT32840
17	856.2	50.6	878	11	AD192744
18	856.2	50.6	878	12	ADK44034
19	720	42.6	934	4	AAI97882
20	632.6	35.9	631	5	AAAF6618
21	606.6	35.9	631	5	AAAF6618

22	606.6	35.9	631	6	ABK38529	ABK38529 CDNA enco
23	606.6	35.9	631	8	ACA10858	ACA10858 Human lun
24	606.6	35.9	631	8	ABX99809	ABX99809 Lung canc
25	606.6	35.9	631	10	ADH46072	ADH46072 Human lun
26	606.6	35.9	631	12	ADH71824	ADH71824 Human lun
27	596.4	35.3	955	4	AAI97781	AAI97781 Human neu
28	572.8	33.9	784	6	ABK39620	ABK39620 CDNA enco
29	572.8	33.9	784	6	ACA11949	ACA11949 Human lun
30	572.8	33.9	784	8	ACA03135	ACA03135 Lung canc
31	572.8	33.9	784	10	ADH47177	ADH47177 Human lun
32	543.4	32.1	576	5	AAE68722	AAE68722 Human lun
33	543.4	32.1	576	6	ABK38633	ABK38633 CDNA enco
34	543.4	32.1	576	8	ACA10962	ACA10962 Human lun
35	543.4	32.1	576	8	ABX99913	ABX99913 Lung canc
36	543.4	32.1	576	10	ADH46176	ADH46176 Human lun
37	543.4	32.1	576	12	ADH71928	ADH71928 Human lun
38	516.4	30.5	571	6	ABO59256	ABO59256 Human col
39	491.4	29.1	817	6	ABL99979	ABL99979 Rat disea
40	442.8	26.2	543	6	ABL99975	ABL99975 Rat disea
41	426.4	25.2	663	10	ADP44700	ADP44700 Human NOV
42	423.8	25.1	427	9	ACH18609	ACH18609 Human adu
43	423.2	25.0	663	12	ADO50885	ADO50885 Human NOV
44	413	24.4	459	9	ACH26489	ACH26489 Human adu
45	383.8	22.7	411	9	ACH29910	ACH29910 Human tes

ALIGNMENTS

RESULT 1	AAZ36910	standard; CDNA; 1691 BP.
ID	AAZ36910	
XX	XX	
AC	AAZ36910;	
XX	XX	
DT	13-MAR-2000	(first entry)
XX	XX	
DE	CDNA encoding a regulator of G protein signalling RGSS.	
XX	XX	
KM	Activator of G protein signalling; AGS; ras-related G protein;	
KM	GTP hydrolysis; G protein activity; pheromone response pathway;	
KM	G protein-coupled signal transduction; G-gamma selectivity;	
KM	cellular signal transduction; regulator of G protein signalling; RGSS;	
XX	se.	
OS	Homo sapiens.	
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	45..590
FT	FT	/*tag= a
XX	XX	/product= "regulator of G-protein signalling"
PN	W09958670-A1.	
XX	XX	
PD	18-NOV-1999.	
XX	XX	
PF	07-MAY-1999;	99WO-US010151.
XX	XX	
PR	08-MAY-1998;	98US-0084842P.
XX	XX	
PR	07-OCT-1998;	98US-0103355P.
XX	XX	
PA	(CADU-) CADUS PHARM CORP.	
XX	XX	
PI	Cismowski M, Duzic E;	
XX	XX	
DR	WPI; 2000-072337/06.	
XX	XX	
DR	P-BSD; AA153931.	
XX	XX	
PT	A new activator of G protein signalling used to treat disorders	
XX	XX	
PT	characterized by an aberrant AGS protein activity.	
XX	XX	
PS	Claim 73; Page 139-140; 162pp; English.	
XX	XX	

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OM protein - protein search, using sw model

Run on: January 12, 2005, 16:32:26 ; Search time 112.522 Seconds
(without alignments)
895.854 Million cell updates/sec

Title: US-10-804-491-2

Perfect score: 1449
Sequence: 1 MKLAMIRKMCPSDELSIP.....IREKASAGSQAKXKRCVYS 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1449	100.0	281	2	AA142693 Human Kd3
2	1449	100.0	281	3	AA153924 An activa
3	1449	100.0	281	3	AA153924 A human a
4	1449	100.0	281	3	ABR41059 Human MAP
5	1441	99.4	281	6	AA199656 Human GTP
6	1399.5	96.6	280	2	AA142694 Rat Kd312
7	893	61.6	278	3	AA153923 A homolo
8	893	61.6	278	5	ABR90722 Human Tum
9	893	61.6	278	6	ABU54429 Human Tum
10	893	61.6	278	8	AD167005 Human DEX
11	893	61.6	278	8	ADQ17642 Human scf
12	893	61.6	278	8	ADQ17642 Human scf
13	889	61.4	266	5	ABR90733 Human DIT
14	889	61.4	266	6	ABU54440 Human Tum
15	879	60.7	266	5	ABG70951 Human Ras
16	863	59.6	266	6	ABR90781 Mouse Tum
17	863	59.6	266	6	ABU54488 Mouse Tum
18	719	49.6	293	4	ABG26384 Novel hum
19	615	42.4	434	4	ABR60711 Drosophi
20	517	35.7	175	8	ABO58923 Human gen
21	425	29.3	82	7	AD135028 Ras-like
22	334	23.1	199	4	AA139896 Human pol
23	334	23.1	199	5	AAE23389 Human pol
24	334	23.1	206	4	AA141682 Human pol
25	330.5	22.8	319	4	ABR68087 Drosophi

26	327	22.6	214	7	ADE09235 Novel pro
27	326	22.5	198	6	ABU62878 Human ras
28	326	22.5	238	6	ABU11837 Human MDD
29	326	22.5	253	7	ADE08246 Novel pro
30	322	22.2	293	5	ABP51431 Human MDD
31	307.5	21.2	233	4	ABR63896 Drosophi
32	305	21.0	183	8	AD135821 Human BAS
33	305	21.0	183	8	ADN05368 Human BAS
34	305	21.0	215	4	AA100956 Antipso
35	301	20.8	183	2	AA100956 Human bon
36	301	20.8	183	4	AA100956 RAPIA Gen
37	301	20.8	183	6	AA100956 Human pol
38	301	20.8	183	7	ABU62883 Ras-famil
39	301	20.8	203	2	AA14201 Human src
40	301	20.8	203	2	AA14201 Human TC2
41	301	20.8	204	6	ABR41057 Human MAP
42	301	20.8	204	6	ABR41056 Human MAP
43	301	20.8	204	7	AD169435 Human hea
44	301	20.8	204	8	AD19894 Human PRO
45	301	20.8	288	4	AD19631 Human PRO
					Aag74576 Human col

ALIGNMENTS

RESULT 1	
AA142693	
ID	AA142693 standard; protein; 281 AA.
XX	
AC	AA142693;
XX	
DT	17-JAN-2000 (first entry)
XX	
DE	Human kd312 polypeptide.
XX	
KM	kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;
KW	heart attack; head trauma; neurodegenerative disease; human;
KW	Parkinson's disease; Alzheimer's disease.
XX	
OS	Homo sapiens.
XX	
FN	W09950288-A2.
XX	
PD	07-OCT-1999.
XX	
PF	30-MAR-1999; 99WO-US006993.
XX	
FR	31-MAR-1998; 98US-00053374.
XX	
XX	(AMGE-) AMGEN INC.
XX	
PI	Yen K;
XX	
DR	WPI; 1999-601322/51.
DR	N-PSDB; AA223022; AA223023.
PT	kd312 polypeptides useful for treating diseases and disorders associated
PT	with alterations in cell proliferation and cell death.
XX	
PS	Claim 10; Fig 5; 85pp; English.
XX	
CC	The invention provides nucleic acid molecules encoding human and rat
CC	kd312 polypeptides. The kd312 polypeptides can be expressed by strand
CC	recombinant methodology. The kd312 sequences, and the antibodies against
CC	the proteins may be used to treat or diagnose the presence or progression
CC	of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
CC	stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
CC	Parkinson's disease and Alzheimer's disease). The present sequence
XX	represents the human kd312 polypeptide
XX	
SO	Sequence 281 AA;
Query Match	100.0%; Score 1449; DB 2; Length 281;

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OW protein - protein search, using sw model

Run on: January 12, 2005, 16:38:13 ; Search time 27.9784 Seconds
(without alignments)
966.351 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAMIKMKCPDSELSIP.....IREKASAGQAKDKRCVIS 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: .pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	314.5	21.7	217	1 TVWYRS	transforming prote
2	306	21.1	183	1 TVHUR2	transforming prote
3	303	20.9	219	2 T15833	hypothetical prote
4	301	20.8	183	2 S03180	transforming prote
5	296.5	20.5	215	1 TVHUC2	GRP-binding protei
6	290.5	20.0	219	2 JN0562	hypothetical 24K p
7	289.5	20.0	219	2 T45545	transforming prote
8	288.5	19.9	219	1 S65761	ras-related GTP-bi
9	288.5	19.9	219	1 TVWYRS	transforming prote
10	288.5	19.9	425	2 T25549	hypothetical prote
11	287	19.8	186	2 A37355	transforming prote
12	286.5	19.8	192	2 S32042	GRP-binding protei
13	285.5	19.7	186	1 TVDORS	transforming prote
14	285.5	19.7	186	2 S11229	GRP-binding protei
15	285.5	19.7	212	2 A53778	GRP-binding protei
16	283.5	19.6	184	1 A34655	transforming prote
17	283.5	19.6	184	1 TVHUR1	transforming prote
18	283.5	19.6	184	2 P38625	GRP-binding protei
19	283.5	19.6	184	2 A61216	transforming prote
20	283	19.5	188	1 TVWS2K	transforming prote
21	283	19.5	188	2 S34138	transforming prote
22	283	19.5	272	2 A34511	GRP-binding protei
23	282.5	19.5	184	1 A31961	transforming prote
24	282.5	19.5	184	2 A32342	transforming prote
25	282	19.5	188	2 I58402	transforming prote
26	282	19.5	218	1 TVHUR	transforming prote
27	281	19.4	188	2 JCS154	K-ras protein - tu
28	281	19.4	213	2 S12892	transforming prote
29	280.5	19.4	184	2 A41217	transforming prote

30	280	19.3	188	1 TVHUR2K	transforming prote
31	280	19.3	188	2 S31720	transforming prote
32	279.5	19.3	193	2 S38362	Potrac protein - s
33	279	19.3	219	1 TVBYR	ras-like protein 1
34	278.5	19.2	184	2 JCS155	rap1a protein - tu
35	276	19.0	188	2 T19507	hypothetical prote
36	275.5	19.0	189	1 TVCHRS	transforming prote
37	275.5	19.0	189	1 TVHUR	transforming prote
38	274.5	18.9	189	1 TVWYRS	transforming prote
39	274.5	18.9	241	1 TVWYRS	transforming prote
40	274	18.9	189	2 S33796	ras protein homolo
41	273.5	18.9	172	2 A54321	transforming prote
42	273.5	18.9	183	2 S05483	transforming prote
43	273.5	18.9	189	2 A43816	transforming prote
44	273.5	18.9	189	2 A25229	c-H-ras protein
45	272.5	18.8	187	2 A60192	transforming prote

ALIGNMENTS

RESULT 1

TVWYRS
Transforming protein ras - shiitake mushroom
C:Species: Lentinula edodes (shiitake mushroom)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: J06199; J01296
R:Hori, K.; Kajiwara, S.; Saito, T.; Miyazawa, H.; Katayose, Y.; Shishido, K.
Gene 105, 91-96, 1991
A>Title: Cloning, sequence analysis and transcriptional expression of a ras gene of the
A:Reference number: J01296; MUID:92039023; PMID:1937010
A:Accession: J06199
A:Molecule type: DNA
A:Residues: 1-217 <HOR>
A:Cross-references: UNIPROT:P28775; GB:D00742; NID:G217947; PIDN:BAA0642.1; PID:G217947
A>Note: The source was designated as Lentinus edodes
C:Genetics:
A:Gene: ras
A:Introns: 4/3; 20/1; 45/1; 72/2; 137/1; 176/3
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; lipoprotein; membrane protein; methylated carboxyl end; nucleoi
F:11-126/Domain: translation elongation factor Tu homology <RTU>
F:17-24/Region: nucleotide-binding motif A (P-loop)
F:123-126/Region: GTP-binding NKXD motif
F:153-155/Region: GTP-binding SAK/L motif
F:223-24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #str
F:214/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
F:214/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

Query Match 21.7%; Score 314.5; DB 1; Length 217;
Best Local Similarity 35.2%; Pred. No. 6.2e-18;
Matches 80; Conservative 35; Mismatches 67; Indels 45; Gaps 7;

QY	25	YRMVILGSSKVGKTAIVSRFLTGFEEDAYPTIEDFRKRYSSIRGEVYQDILDTSGNHP	84
DB	11	YKLVVVGCGGKALTIQIFQSHFVDEYDPTIEDSVKQCVIDDEVALLDVLTAGQEE	70
QY	85	FPANRRSLITLGDVFLVPSLDNRDSFEVQRARQQLDTRKSLCKTKTENVDVPLVTCG	144
DB	71	YGAREEQYMRGTGEFLVYSITSRNSFEISTHQQL-----RVKQDTPPVVVA	122
QY	145	NKGDRDFYREVDQREIEQLVGDDPQR---CAVEISAKKNSLIDQMFALFAAKLPSEM	201
DB	123	NKCDLEVERGVNME-----GRDLAHFGCKFVETSKRVINVDQAFQ-----	165
QY	202	SPDLHRVSVQYCDVLHKKALRNKKLIRAG---SGGGSGDPGDARF	244
DB	166	--DIVREIR-KY-----NKEQQTGRMMVTGGGGGPPPTVAG	199

RESULT 2

TVHUR2
Transforming protein rap2b - human

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 03:46:36 ; Search time 6984 Seconds
(without alignments)
11450.012 Million cell updates/sec

Title: US-10-804-491-24
Perfect score: 1691
Sequence: 1 taagaagctgctacttaaac.....tcgcaaaaaaaaaaaaaa 1691

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1691	100.0	1691	9	AF159570 Homo sapi
2	1689.4	99.9	2076	9	AB008109 Homo sapi
3	1689.4	99.9	5683	9	BSM805729 Homo sapi
4	1687.8	99.8	2075	6	CO714475 Homo sapi
5	1686.4	99.7	2601	11	BV180396 Homo sapi
6	1676.8	99.2	3208	6	AR454638 Homo sapi
7	1676.4	99.1	1923	6	BD074349 Homo sapi
8	1675.4	99.1	1710	6	BC030059 Homo sapi
9	1587.8	93.9	2190	6	AR380250 Homo sapi
10	1263.8	74.7	165329	9	AL583850 Homo sapi
11	1263.8	74.7	191689	2	AC031977 Homo sapi
12	1105.2	65.4	1285	9	AF030108 Homo sapi
13	856.2	50.6	878	6	AR280577 Sequence
14	856.2	50.6	878	6	AR283073 Sequence
15	856.2	50.6	878	6	AR341846 Sequence
16	856.2	50.6	878	6	AR343841 Sequence
17	856.2	50.6	878	6	AR351042 Sequence
18	856.2	50.6	878	6	AR352808 Sequence
19	856.2	50.6	878	6	AR453622 Sequence

20	856.2	50.6	878	6	AX302762 Sequence
21	825.6	48.8	2078	4	SSC549925 Sequence
22	720	42.6	744	6	AR075100 Sequence
23	720	42.6	744	6	BD091623 Human reg
24	684.4	40.5	857	11	BV166677 RGS5_786
25	632.6	37.4	934	6	BD021619 Novel gen
26	632.6	37.4	934	6	BD101557 Novel gen
27	606.6	35.9	631	6	AR272824 Sequence
28	606.6	35.9	631	6	AR276405 Sequence
29	606.6	35.9	631	6	AR406680 Sequence
30	606.6	35.9	631	6	AR440530 Sequence
31	606.6	35.9	631	6	AR472688 Sequence
32	606.6	35.9	631	6	AX062926 Sequence
33	606.6	35.9	631	6	AX367843 Sequence
34	596.4	35.3	955	6	BD021618 Novel gen
35	596.4	35.3	955	6	BD101556 Novel gen
36	572.8	33.9	784	6	AR273915 Sequence
37	572.8	33.9	784	6	AR277496 Sequence
38	572.8	33.9	784	6	AR407771 Sequence
39	572.8	33.9	784	6	AR441621 Sequence
40	572.8	33.9	784	6	AX368948 Sequence
41	546	32.3	546	9	AF493929 Homo sapi
42	543.4	32.1	576	6	AR272928 Sequence
43	543.4	32.1	576	6	AR276509 Sequence
44	543.4	32.1	576	6	AR406784 Sequence
45	543.4	32.1	576	6	AR440634 Sequence

ALIGNMENTS

RESULT 1	AF159570	1691 bp	mRNA	linear	PRI 10-JAN-2000
LOCUS	AF159570				
DEFINITION	Homo sapiens regulator of G-protein signalling 5 (RGS5) mRNA,				
ACCESSION	AF159570				
VERSION	AF159570.1	GI:5230675			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Fuentezranz,H., Ianier,S.M. and Duzic,E.				
TITLE	Genetic screens in yeast to identify mammalian nonreceptor modulators of G-protein signalling				
JOURNAL	Nat. Biotechnol. 17 (9), 878-883 (1999)				
MEDLINE	99403338				
PUBMED	10471929				
REFERENCE	2 (bases 1 to 1691)				
AUTHORS	Cismowski M.J. and Duzic,E.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-JUN-1999) Receptor Pharmacology/Biochemistry, Cadus Pharmaceutical Corporation, 777 Old Saw Mill River Road, Tarrytown, NY 10591, USA				
FEATURES					
source	location/Qualifiers				
gene	1..1691				
CDS	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/tissue_type="liver"				
	/dev stage="adult"				
	1..1691				
	/gene="RGS5"				
	45..590				
	/gene="RGS5"				
	/codon_start=1				
	/product="regulator of G-protein signalling 5"				
	/protein_id="A040957.1"				
	/db_xref="GI:5230676"				
	/translation="MCKGLALPHSCERAKEIKIKIGILQKPDSDVIVPNEKP				

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OM protein - protein search, using sw model

Run on: January 12, 2005, 16:32:21 ; Search time 114.955 Seconds

(without alignments)
1406.471 Million cell updates/sec

Title: US-10-804-491-2

Perfect score: 1449

Sequence: 1 MRLAMIKMKCPDSELSIP.....IREKASAGSQAXDKKRCVIS 281

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_02:*

2: uniprot_sprot:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1449	100.0	281	1 RASD_HUMAN	O9y272 homo sapien
2	1405.5	97.0	280	1 RASD_MOUSE	O35626 mus musculu
3	1399.5	96.6	280	1 RASD_RAT	O9jkr8 rattus norv
4	1144.5	79.0	265	1 O6PHV8	O6phv8 brachydanio
5	1144.5	79.0	265	2 AAH56272	AAH56272 brachydan
6	996	68.7	184	2 O9HC43	O9hc43 homo sapien
7	896	61.8	266	2 O6GM99	O6gm99 xenopus lae
8	889	61.4	266	1 RHES_HUMAN	O96d21 homo sapien
9	889	61.4	266	2 CAG30363	Cag30363 homo sapi
10	867	59.8	317	2 O8JZW1	O8jzw1 mus musculu
11	863	59.6	266	1 RHES_MOUSE	O9wv43 mus musculu
12	615	42.4	454	2 O9VSI0	O9vsi0 drosophila
13	359	24.8	306	2 O9WSG7	O9wsg7 drosophila
14	352.5	24.3	199	2 O7OHQ9	O7ohq9 anopheles g
15	341	23.5	199	2 O6GM41	O6gm41 xenopus lae
16	339	23.4	195	2 O803Y2	O803y2 brachydanio
17	335	23.1	199	2 O9SKD9	O9skd9 macaca fasc
18	334	23.1	199	2 O96HD8	O96hd8 homo sapien
19	334	23.1	199	2 O7TQ15	O7tq15 mus musculu
20	326	22.5	198	2 O9V857	O9v857 homo sapien
21	325.5	22.5	198	2 O9V986	O9v986 drosophila
22	325.5	22.5	198	2 AAF57410	AAf57410 drosophi
23	321	22.2	198	2 O91Z61	O91z61 mus musculu
24	321	22.2	198	2 AAH57556	AAh57556 mus muscu
25	318.5	22.0	280	2 O8WQD0	O8wqd0 drosophila
26	314.5	21.7	1	1 RASD_LENED	P28775 leninula e
27	312.5	21.6	332	2 O02139	O02139 caenorhabdi
28	309	21.3	182	2 O6NSJ3	O6nsj3 xenopus lae
29	309	21.3	182	2 O7SV59	O7sv59 brachydanio
30	309	21.3	182	2 AAH70538	AAh70538 xenopus l
31	309	21.3	182	2 AAH28683	AAh28683 xenopus l

32	309	21.3	182	2	AAH35575	AAh35575 xenopus l
33	308.5	21.3	209	2	O8AYE6	O8aye6 xenopus lae
34	307.5	21.2	233	2	O9VH66	O9vh66 drosophila
35	305	21.0	183	1	RP2B_HUMAN	P61225 homo sapien
36	305	21.0	183	1	RP2B_MOUSE	P61226 mus musculu
37	305	21.0	183	1	RP2B_RAT	P61227 rattus norv
38	305	21.0	183	2	O6NRU1	O6nru1 xenopus lae
39	305	21.0	183	2	O7ZX67	O7zx67 xenopus lae
40	305	21.0	183	2	AAH46528	AAh46528 mus muscu
41	305	21.0	183	2	BAC31411	Bac31411 mus muscu
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43	305	21.0	183	2	AAH70626	AAh70626 xenopus l
44	305	21.0	183	2	AAH35578	AAh35578 xenopus l
45	303	20.9	183	2	O9BTS0	O9bts0 homo sapien

ALIGNMENTS

RESULT 1
RASD_HUMAN STANDARD; PRT; 281 AA.
ID RASD_HUMAN
AC O9y272; O9NYB4;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dexamethasone-induced Ras-related protein 1 (Activator of G-protein
signaling 1).
GN Name=RASD1; Synonyms=DEXRASI, AGS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RA Kempainen R.J.;
RT "Identification of human pituitary Dexamet.
Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
[2]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INDUCTION.
RX MEDLINE=20135605; PubMed=10673050; DOI=10.1016/S0167-4781(99)00197-9;
RA Tu Y., Wu C.;
RT "Cloning, expression and characterization of a novel human Ras-related
protein that is regulated by glucocorticoid hormone."
Biochim. Biophys. Acta 1489:452-456(1999).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=99403338; PubMed=10471929;
RA Cismowski M.J., Takesono A., Ma C., Lizano J.S., Xie X.,
Puerkhanz H., Lanier S.M., Duzic E.;
RT "Genetic screens in yeast to identify mammalian nonreceptor modulators
of G-protein signaling."
Nat. Biotechnol. 17:878-883(1999).
[4]
RP SEQUENCE FROM N.A.
RX Cismowski M.J., Xie X., Duzic E.;
RT "Genomic sequence of the human ras-related G-protein activator AGS1."
Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC Kempainen R.J., Behrend E.N.;
RT "Human Dexamet gene."
Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Puhl H.T., Ikeda S.R., Aronstam R.S.;
RT Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

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OM protein - protein search, using sw model

Run on: January 12, 2005, 18:34:53 ; Search time 678.171 Seconds
(without alignments)
149.700 Million cell updates/sec

Title: US-10-804-491-2

Perfect score: 1449

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1449	100.0	281	US-10-804-491-46	Sequence 46, App1
5	893	61.6	278	US-09-918-715-178	Sequence 178, App
6	893	61.6	278	US-10-804-491-41	Sequence 41, App1
7	893	61.6	278	US-10-474-794-178	Sequence 178, App
8	893	61.6	278	US-10-723-860-459	Sequence 459, App
9	889	61.4	266	US-09-778-963A-4	Sequence 4, App1
10	889	61.4	266	US-09-918-715-198	Sequence 198, App
11	879	60.7	266	US-10-474-794-198	Sequence 198, App
12	879	60.7	266	US-09-778-963A-2	Sequence 2, App1
13	863	59.6	266	US-09-778-963A-5	Sequence 5, App1

14	863	59.6	266	10	US-09-918-715-293	Sequence 293, App
15	863	59.6	266	17	US-10-474-794-293	Sequence 293, App
16	517	35.7	175	14	US-10-029-386-32557	Sequence 32557, A
17	334	23.1	199	16	US-10-399-455-16	Sequence 16, App1
18	326	22.5	198	10	US-09-873-546-5	Sequence 5, App1
19	322	22.2	293	16	US-10-363-829-453	Sequence 453, App
20	305	21.0	183	15	US-10-231-956A-429	Sequence 429, App
21	303	20.9	219	14	US-10-369-493-5393	Sequence 5393, Ap
22	301	20.8	183	9	US-09-482-520A-8	Sequence 8, App1
23	301	20.8	183	9	US-09-873-546-12	Sequence 12, App1
24	301	20.8	203	14	US-10-197-666A-84	Sequence 84, App1
25	301	20.8	204	14	US-10-197-666A-82	Sequence 82, App1
26	301	20.8	204	16	US-10-408-765A-1241	Sequence 1241, Ap
27	301	20.8	204	16	US-10-322-281-474	Sequence 474, App
28	301	20.8	204	17	US-10-788-792-208	Sequence 208, App
29	301	20.8	204	17	US-10-788-792-209	Sequence 209, App
30	301	20.8	214	16	US-10-322-281-467	Sequence 467, App
31	301	20.8	288	14	US-10-106-598-5350	Sequence 5350, App
32	301	20.8	734	15	US-10-344-404-31	Sequence 31, App1
33	301	20.8	758	15	US-10-344-404-36	Sequence 36, App1
34	300	20.7	183	16	US-10-755-889-82	Sequence 82, App1
35	300	20.7	190	9	US-09-764-868-680	Sequence 680, App
36	299.5	20.7	745	15	US-10-344-404-19	Sequence 19, App1
37	291	20.1	175	9	US-09-764-868-1103	Sequence 1103, Ap
38	288.5	19.9	740	15	US-10-344-404-12	Sequence 12, App1
39	288.5	19.9	764	15	US-10-344-404-34	Sequence 34, App1
40	286.5	19.8	740	15	US-10-344-404-27	Sequence 27, App1
41	283.5	19.6	184	16	US-10-408-765A-856	Sequence 856, App
42	283.5	19.6	184	16	US-10-322-281-78	Sequence 78, App1
43	283	19.5	188	16	US-10-738-546A-5	Sequence 5, App1
44	283	19.5	272	14	US-10-369-493-21983	Sequence 21983, A
45	282.5	19.5	184	10	US-09-873-546-11	Sequence 11, App1

ALIGNMENTS

RESULT 1
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; Sequence 88, Application US/10197666A
; Publication No. US20030092037A1
GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSIKI KAISYA
; TITLE OF INVENTION: Elki phosphorylation related gene
; FILE REFERENCE: PH-1548US
; CURRENT APPLICATION NUMBER: US/10/197,666A
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: JP 2001-218204
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: JP 2001-263450
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2002-012176
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 60/305,884
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/316,304
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 60/350,027
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-197-666A-88

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Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MKLAMIKMCPSELSIPAKNCRMVITLSSKVGKTAIYSRPLTGFEDAYPTTIDF 60
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2005, 18:15:29 ; Search time 35.8653 Seconds
(without alignments)
519.304 Million cell updates/sec

Title: US-10-804-491-2
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	1449	100.0	281	US-09-439-410A-46	Sequence 46, Appli
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9	893	61.6	278	US-09-709-103-41	Sequence 41, Appli
10	893	61.6	278	US-09-439-410A-41	Sequence 41, Appli
11	311	21.5	60	US-09-439-410A-109	Sequence 109, App
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13	306	21.1	183	US-08-718-270A-39	Sequence 39, Appli
14	305	21.0	60	US-09-439-410A-82	Sequence 82, Appli
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16	301	20.8	183	US-09-482-520A-8	Sequence 8, Appli
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23	288	19.9	213	US-09-503-505A-3	Sequence 3, Appli
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26	285	19.7	187	US-09-078-317-11	Sequence 11, Appli
27	283	19.5	55	US-09-439-410A-117	Sequence 117, App

28	282	19.5	183	3	US-09-078-317-13	Sequence 13, Appli
29	282	19.5	183	4	US-09-454-818-13	Sequence 13, Appli
30	282	19.5	210	3	US-09-053-374A-7	Sequence 7, Appli
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32	281	19.4	218	1	PCT-US95-06420-3	Sequence 3, Appli
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34	280.5	19.4	184	2	US-08-718-270A-43	Sequence 43, Appli
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36	277.5	19.2	189	2	US-08-884-866A-6	Sequence 6, Appli
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38	275.5	19.0	160	3	US-08-884-866A-7	Sequence 7, Appli
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45	275.5	19.0	189	3	US-09-209-668-11	Sequence 11, Appli

ALIGNMENTS

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RESULT 1
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; Sequence 2, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,374A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-053-374A-2
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